Features	**p-value**	**Persistent mean**	**Recent mean**	**Description**	**Dynamics in time**	**Interpretation**
1. Mean distance	1·41E-24	0·034	0·015	Average number of point mutations between pairs of haplotypes. Measures diversity	↑	Accumulation of mutations and diversification over the course of intra-host evolution
2. Std distance	4·10E-14	0·019	0·010	Standard deviation of number of point mutations between pairs of haplotypes. Measures diversity.	↑	
3. Conservation score	5·11E-25	0·422	0·188	Average distance between the observed nucleotides and their consensuses. The distance is based on the NUC44 scoring matrix. Measures diversity	↑	
4. Mutation frequency	3·07E-16	0·023	0·010	Average number of point mutations between haplotypes and the most frequent haplotype. Measures diversity.	↑	
5. k-entropy E_k(k=10)	7·00E-23	0·630	0·357	Average entropy of k-mers	↑	

				(subsequences of length k) starting at fixed genomic positions. Measures diversity.		
6. Frequency entropy E_L	4·56E-06	0·668	0·567	Entropy of observed haplotype frequencies. Measures diversity.	↑	
7. SNV entropy E_1	1·14E-21	0·084	0·043	Average entropy of SNV frequencies. Measures diversity.	↑	
8. Transversion mutation	1·06E-07	0·061	0·032	Frequency of mutations between purine and pyrimidine nucleotides.	↑	The role of genetic saturation
9. DN/DS	5·39E-10	0·713	1·330	Ratio of non-synonymous (DN) and synonymous (DS) substitutions. Measures the strength of selection	↓	Increase in purifying selection indicating a growing role of intra-host adaptation
10. PCA complexity	1·4E-03	0·0053	0·0125	Percentage of principal components required to explain at least α=50% percent of the observed genetic variance. Measures the	↓	Increase of structuredness of intra-host viral populations, possibly associated with intra-host adaptation and

				population complexity.		emergence of specialization
11. Kolmogorov complexity	1·55E-11	0·041	0·052	The highest possible degree of compression of observed viral sequences without loss of information. Measures the population complexity.	↓	
12.Robustness/Selection balance	3·66E-15	0·628	0·386	Correlation between haplotype frequencies and haplotype centralities in the observed genetic network. Measures the balance between mutational robustness and selection.	↑	The major role of multiple founders at the earlier infection stage, later superseded by the increased role of mutational robustness.
13. s-metric	1·93E-20	0·001	0·044	Network theory feature that measures how close a genetic network is to being scale-free (a type of networks characterized by the presence of hubs, small diameter and a power-law degree distribution)	↓	

14. Clustering coefficient	2·08E-13	0·082	0·356	Network theory feature that measures the propensity of haplotypes to cluster together in the genetic network	↓	
15. ODE feature C_{ODE}	2·42E-06	-0·270	0·224	The estimation of a population age using a dynamic model of viral evolution under the immune system's pressure.	N/A	Declining role of immune escape
16. Biochemical feature	2·92E-35	0·628	0·379	Total frequency of haplotypes identified as having a physico-chemical profile pointing to persistent infection.	↑	The change of physico-chemical properties is likely to be associated with transition between evolutionary mechanisms responsible for virus survival and proliferation at different infection stages. .

Table S1*: Descriptions and statistical results for analyzed features.*